

PCT09

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/831,050

TIME: 14:10:22

Input Set : A:\seqlist_1581.0800000

Output Set: N:\CRF3\11142001\I831050.raw

6 <110> APPLICANT: SHONE, Clifford Charles
7 SUTTON, John Mark
8 HALLIS, Bassam
9 SILMAN, Nigel
11 <120> TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
13 <130> FILE REFERENCE: 1581.0800000
15 <140> CURRENT APPLICATION NUMBER: 09/831,050
16 <141> CURRENT FILING DATE: 1999-11-05
18 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03699
19 <151> PRIOR FILING DATE: 1998-11-05
21 <160> NUMBER OF SEQ ID NOS: 11
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 204
27 <212> TYPE: PRT
28 <213> ORGANISM: Bacillus caldotenax
30 <400> SEQUENCE: 1

31	Met	Pro	Phe	Glu	Leu	Pro	Ala	Leu	Pro	Tyr	Pro	Tyr	Asp	Ala	Leu	Glu
32	1				5					10					15	
34	Pro	His	Ile	Asp	Lys	Glu	Thr	Met	Asn	Ile	His	His	Thr	Lys	His	His
35				20					25					30		
37	Asn	Thr	Tyr	Val	Thr	Asn	Leu	Asn	Ala	Ala	Leu	Glu	Gly	His	Pro	Asp
38			35				40						45			
40	Leu	Gln	Asn	Lys	Ser	Leu	Glu	Leu	Leu	Ser	Asn	Leu	Glu	Ala	Leu	
41		50				55					60					
43	Pro	Glu	Ser	Ile	Arg	Thr	Ala	Val	Arg	Asn	Asn	Gly	Gly	Gly	His	Ala
44		65			70				75						80	
46	Asn	His	Ser	Leu	Phe	Trp	Thr	Ile	Leu	Ser	Pro	Asn	Gly	Gly	Gly	Glu
47				85					90						95	
49	Pro	Thr	Gly	Glu	Leu	Ala	Glu	Ala	Ile	Asn	Lys	Lys	Phe	Gly	Ser	Phe
50			100					105						110		
52	Thr	Ala	Phe	Lys	Asp	Glu	Phe	Ser	Lys	Ala	Ala	Ala	Gly	Arg	Phe	Gly
53			115					120					125			
55	Ser	Gly	Trp	Ala	Trp	Leu	Val	Val	Asn	Asn	Gly	Glu	Leu	Glu	Ile	Thr
56		130				135						140				
58	Ser	Thr	Pro	Asn	Gln	Asp	Ser	Pro	Ile	Met	Glu	Gly	Lys	Thr	Pro	Ile
59		145			150					155					160	
61	Leu	Gly	Leu	Asp	Val	Trp	Glu	His	Ala	Tyr	Tyr	Leu	Lys	Tyr	Gln	Asn
62				165					170						175	
64	Arg	Arg	Pro	Glu	Tyr	Ile	Ala	Ala	Phe	Trp	Asn	Ile	Val	Asn	Trp	Asp
65			180						185					190		
67	Glu	Val	Ala	Lys	Arg	Tyr	Ser	Glu	Ala	Lys	Ala	Lys				
68		195						200								

72 <210> SEQ ID NO: 2
73 <211> LENGTH: 204
74 <212> TYPE: PRT
75 <213> ORGANISM: Bacillus stearothermophilus

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77 <400> SEQUENCE: 2

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78 Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu
79   1           5           10           15
81 Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
82           20           25           30
84 Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
85           35           40           45
87 Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
88           50           55           60
90 Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
91   65           70           75           80
93 Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
94           85           90           95
96 Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe
97           100          105          110
99 Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
100          115          120          125
102 Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr
103          130          135          140
105 Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
106          145          150          155          160
108 Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn
109           165           170           175
111 Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Val Val Asn Trp Asp
112           180           185           190
114 Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys
115           195           200

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119 <210> SEQ ID NO: 3

120 <211> LENGTH: 1067

121 <212> TYPE: PRT

122 <213> ORGANISM: Artificial Sequence

124 <220> FEATURE:

125 <223> OTHER INFORMATION: Description of Artificial Sequence:construct *OK*

127 <400> SEQUENCE: 3

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128 Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu
129   1           5           10           15
131 Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
132           20           25           30
134 Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
135           35           40           45
137 Leu Gln Asn Lys Ser Leu Glu Glu Leu Leu Ser Asn Leu Glu Ala Leu
138           50           55           60
140 Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
141   65           70           75           80
143 Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
144           85           90           95
146 Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe
147           100          105          110
149 Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly

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150          115          120          125
152 Ser Gly Trp Ala Trp Leu Val Asn Asn Gly Glu Leu Glu Ile Thr
153          130          135          140
155 Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
156 145          150          155          160
158 Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn
159          165          170          175
161 Arg Arg Pro Glu Tyr Ile Ala Ala Phe Trp Asn Val Val Asn Trp Asp
162          180          185          190
164 Glu Val Ala Lys Arg Tyr Ser Glu Ala Lys Ala Lys Gln Arg Ser Cys
165          195          200          205
167 Gly Leu Val Pro Arg Gly Ser Gly Pro Gly Ser Ala Leu Asn Asp Leu
168          210          215          220
170 Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp
171 225          230          235          240
173 Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr
174          245          250          255
176 Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln
177          260          265          270
179 Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile
180          275          280          285
182 Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn
183          290          295          300
185 Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr
186 305          310          315          320
188 Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg
189          325          330          335
191 Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg
192          340          345          350
194 Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala
195          355          360          365
197 Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp
198          370          375          380
200 Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp
201 385          390          395          400
203 Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn
204          405          410          415
206 Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala
207          420          425          430
209 Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly
210          435          440          445
212 Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln
213          450          455          460
215 Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val
216 465          470          475          480
218 Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile
219          485          490          495
221 Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu
222          500          505          510

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224  Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu
225          515                      520                      525
227  Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu
228          530                      535                      540
230  Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn
231          545                      550                      555                      560
233  Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val
234          565                      570                      575
236  Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys
237          580                      585                      590
239  Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu
240          595                      600                      605
242  Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu
243          610                      615                      620
245  Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr
246          625                      630                      635                      640
248  Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser
249          645                      650                      655
251  Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly
252          660                      665                      670
254  Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe
255          675                      680                      685
257  Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val
258          690                      695                      700
260  Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile
261          705                      710                      715                      720
263  Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile
264          725                      730                      735
266  Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly
267          740                      745                      750
269  Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val
270          755                      760                      765
272  Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg
273          770                      775                      780
275  Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile
276          785                      790                      795                      800
278  Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly
279          805                      810                      815
281  Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg
282          820                      825                      830
284  Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys
285          835                      840                      845
287  Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn
288          850                      855                      860
290  Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys
291          865                      870                      875                      880
293  Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val
294          885                      890                      895
296  Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly

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297          900          905          910
299 Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly
300          915          920          925
302 Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile
303          930          935          940
305 Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys
306          945          950          955          960
308 Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile
309          965          970          975
311 Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val
312          980          985          990
314 Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met
315          995          1000          1005
317 Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His
318          1010          1015          1020
320 Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg
321          1025          1030          1035          1040
323 Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile
324          1045          1050          1055
326 Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
327          1060          1065
331 <210> SEQ ID NO: 4
332 <211> LENGTH: 1070
333 <212> TYPE: PRT
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence:construct OK
339 <400> SEQUENCE: 4
340 Met Pro Phe Glu Leu Pro Ala Leu Pro Tyr Pro Tyr Asp Ala Leu Glu
341   1          5          10          15
343 Pro His Ile Asp Lys Glu Thr Met Asn Ile His His Thr Lys His His
344          20          25          30
346 Asn Thr Tyr Val Thr Asn Leu Asn Ala Ala Leu Glu Gly His Pro Asp
347          35          40          45
349 Leu Gln Asn Lys Ser Leu Glu Leu Leu Ser Asn Leu Glu Ala Leu
350          50          55          60
352 Pro Glu Ser Ile Arg Thr Ala Val Arg Asn Asn Gly Gly Gly His Ala
353          65          70          75          80
355 Asn His Ser Leu Phe Trp Thr Ile Leu Ser Pro Asn Gly Gly Gly Glu
356          85          90          95
358 Pro Thr Gly Glu Leu Ala Asp Ala Ile Asn Lys Lys Phe Gly Ser Phe
359          100          105          110
361 Thr Ala Phe Lys Asp Glu Phe Ser Lys Ala Ala Ala Gly Arg Phe Gly
362          115          120          125
364 Ser Gly Trp Ala Trp Leu Val Val Asn Asn Gly Glu Leu Glu Ile Thr
365          130          135          140
367 Ser Thr Pro Asn Gln Asp Ser Pro Ile Met Glu Gly Lys Thr Pro Ile
368          145          150          155          160
370 Leu Gly Leu Asp Val Trp Glu His Ala Tyr Tyr Leu Lys Tyr Gln Asn

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VERIFICATION SUMMARY

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